

=====

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=29; hr=17; min=14; sec=58; ms=546; ]

=====

\*\*\*\*\*

Reviewer Comments:

<110> ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY  
MELNICK, Ari M.  
LICHT, Jonathan D.  
PRIVÉ, Gilbert G.  
AHMAD, Khaja Farid

Please remove the foreign accent mark from the fourth applicant's name:  
foreign accent marks are non-ASCII characters, and cannot be processed.

<210> 10  
<211> 17  
<212> PRT  
<213> Artificial

<220>  
<223> consensus sequence

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> amino acid residue is Leu, Gly, or Tyr

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> amino acid residue is Val, Ile, or Arg

<220>  
<221> MISC\_FEATURE

<222> (3)..(3)  
<223> amino acid residue is Ala, Thr, or Ser

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> amino acid residue is Thr or Glu

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> amino acid residue is Val or Ile

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> amino acid residue is Lys or Ile

<220>  
<221> MISC\_FEATURE  
<222> (7)..(7)  
<223> amino acid residue is Glu or Ser

<220>  
<221> MISC\_FEATURE  
<222> (8)..(8)  
<223> amino acid residue is Ala, Met, or Thr

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> amino acid residue is Gly or Ala

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> amino acid residue is Arg or Pro

<220>  
<221> MISC\_FEATURE  
<222> (12)..(12)  
<223> amino acid residue is Ile or Ser

```
<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> amino acid residue is His or Trp
```

```
<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> amino acid residue is Glu or Val
```

```
<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> amino acid residue is Ile or Val
```

```
<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> amino acid residue is Arg or Gly
```

```
<400> 10
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ala | Thr | Val | Lys | Glu | Ala | Gly | Arg | Ser | Ile | His | Glu | Ile | Pro |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |

Arg

The above <220>-<223> sections stating that the amino acids at those locations can also represent another amino acid are incorrect (e.g., for location 1, amino acid residue is Leu, Gly, or Tyr). "Leu" at location 1 can only represent itself. Please use "Xaa's" instead, and explain which amino acid residues they can represent.

```
*****
```

Application No: 10582662

Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2008-05-28 14:21:46.010  
**Finished:** 2008-05-28 14:21:47.829  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 819 ms  
**Total Warnings:** 20  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 34  
**Actual SeqID Count:** 34

| Error code | Error Description                                   |
|------------|---|
| W 213      | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (18) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (20) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (21) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (22) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (23) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (24) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (25) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (26) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (27) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (28) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (29) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (30) |

**Input Set:**

**Output Set:**

**Started:** 2008-05-28 14:21:46.010  
**Finished:** 2008-05-28 14:21:47.829  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 819 ms  
**Total Warnings:** 20  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 34  
**Actual SeqID Count:** 34

**Error code**

**Error Description**

This error has occurred more than 20 times, will not be displayed

<210> 1  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 1

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro  
1 5 10 15

Arg

<210> 2  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 2

Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro  
1 5 10 15

Arg

<210> 3  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 3

Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val Pro  
1 5 10 15

Gly

<210> 4  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 4

Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Glu Glu Leu

<210> 5  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 5

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Gln Asp Ile  
20

<210> 6  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 6

Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val  
1 5 10 15

Pro Gly Pro Ser Pro  
20

<210> 7  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 7

Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu Pro Leu  
20 25

<210> 8  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 8

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr  
20 25

<210> 9  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 9

Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val  
1 5 10 15

Pro Gly Pro Ser Pro Asn Glu Glu Asn Asn Gly Lys  
20 25

<210> 10  
<211> 17  
<212> PRT  
<213> Artificial

<220>  
<223> consensus sequence

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> amino acid residue is Leu, Gly, or Tyr

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> amino acid residue is Val, Ile, or Arg

<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> amino acid residue is Ala, Thr, or Ser

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> amino acid residue is Thr or Glu

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> amino acid residue is Val or Ile

<220>  
<221> MISC\_FEATURE

<222> (6)..(6)  
<223> amino acid residue is Lys or Ile

<220>  
<221> MISC\_FEATURE  
<222> (7)..(7)  
<223> amino acid residue is Glu or Ser

<220>  
<221> MISC\_FEATURE  
<222> (8)..(8)  
<223> amino acid residue is Ala, Met, or Thr

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> amino acid residue is Gly or Ala

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> amino acid residue is Arg or Pro

<220>  
<221> MISC\_FEATURE  
<222> (12)..(12)  
<223> amino acid residue is Ile or Ser

<220>  
<221> MISC\_FEATURE  
<222> (13)..(13)  
<223> amino acid residue is His or Trp

<220>  
<221> MISC\_FEATURE  
<222> (14)..(14)  
<223> amino acid residue is Glu or Val

<220>  
<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> amino acid residue is Ile or Val

<220>  
<221> MISC\_FEATURE  
<222> (17)..(17)  
<223> amino acid residue is Arg or Gly

<400> 10

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro  
1 5 10 15

Arg

<210> 11  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 11

Met Ala Ser Pro Ala Asp Ser Cys Ile Gln Phe Thr Arg His Ala Ser  
1 5 10 15

Asp Val Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr  
20 25 30

Asp Val Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr  
35 40 45

Val Leu Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln  
50 55 60

Leu Lys Cys Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro  
65 70 75 80

Glu Gly Phe Cys Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn  
85 90 95

Leu Arg Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu  
100 105 110

Gln Met Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser  
115 120 125

Glu

<210> 12  
<211> 127  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic mutant

<400> 12

Gly Ser Ala Asp Ser Gln Ile Gln Phe Thr Arg His Ala Ser Asp Val  
1 5 10 15

Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr Asp Val  
20 25 30

Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu  
35 40 45

Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys  
50 55 60

Arg Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly  
65 70 75 80

Phe Asn Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg  
85 90 95

Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met  
100 105 110

Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser Glu  
115 120 125

<210> 13  
<211> 93  
<212> DNA  
<213> Artificial

<220>  
<223> oligonucleotide for plasmid construction

<400> 13  
catggcttgtt ggccacgggt aaggaggggg gcccgtccat ccatgagatc ccgcgcgagg 60  
agctgccccca cacgccccag ctgccccctgg ccc 93

<210> 14  
<211> 93  
<212> DNA  
<213> Artificial

<220>  
<223> oligonucleotide for plasmid construction

<400> 14  
tcgaggggcca ggggcagctc gggcggtgtgc cgcaagtcct cgcgcgggat ctcatggatg 60  
gagcggccccg ccttccttac cgtggccacc agc 93

<210> 15  
<211> 93  
<212> DNA  
<213> Artificial

<220>  
<223> oligonucleotide for plasmid construction

<400> 15  
catggctggg ggcacgggt aaggaggcgg gccgctccat ccatgcagct gcagctgagg 60  
agctgcggca cacgccccag ctgccccctgg ccc 93

<210> 16  
<211> 93  
<212> DNA  
<213> Artificial

<220>  
<223> oligonucleotide for plasmid construction

<400> 16  
tcgaggggcca ggggcagctc gggcggtgc cgcaagtcct cagctgcagc tgcattggatg 60  
gagcggcccg cctccttcaac cgtggccacc agc 93

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 17  
catectgggc cattacctta 20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 18  
tctctctctg catcttgggg 20

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 19  
gactctgaag agccacacctgc 20

<210> 20  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 20  
ctggcttttg tgacggaaat 20

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 21  
ccggaccta tccctcactc 20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 22  
cacaccgatg cagcttctca 20

<210> 23  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 23  
aaaggaaccc cacgaagtgt t 21

<210> 24  
<211> 22

<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 24  
tcaaggccat atcctacaac aa 22

<210> 25  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 25  
acgatgtcg gtcaggtatc 20

<210> 26  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 26  
agtgactagg gcgcgtgttt 20

<210> 27  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 27  
gggttcttag aagtgggtat gc 22

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 28  
tgggactaat cttcggcatt 20

<210> 29  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 29  
cgatgaggag tttcggatg t 21

<210> 30  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 30  
tttctggggg ctctgtggac t 21

<210> 31  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 31  
  
Cys Ala Ile Tyr Arg Ser Glu Ile Ser Thr Ala Pro Ser Ser Trp  
1 5 10 15

Val Val Pro Gly Pro Ser Pro Asn Glu  
20 25

<210> 32  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 32  
  
Arg Ser Glu Ile Ile Ser Thr Ala Pro Ala Ser Ala Val Ala Pro Gly  
1 5 10 15

Pro

<210> 33  
<211> 17

<212> PRT  
<213> Homo sapiens

<400> 33

Arg Ser Glu Ile Ile Ser Thr Ala Pro Trp Ser Ser Val Val Pro Gly  
1 5 10 15

Pro

<210> 34  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 34

Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val Pro Gly  
1 5 10 15

Pro